IN THE SPECIFICATION:

Please amend the Specification at page 33, line 23 through page 34, line 12 in the following manner:

Accordingly, in some embodiments, the present invention provides isolated RNA molecules (double-stranded or single-stranded) that are complementary to sequences required for nematode viability and/or reproduction. In some embodiments, the RNA molecules utilized mediate RNAi for embryonic lethal and sterile genes. Many genes with sterile or embryonic lethal RNAi phenotypes have been identified in high throughput screens (Fraser, A. G., Kamath, R. S., Zipperlen, P., Martinez-Campos, M., Sohrmann, M. and Ahringer, J. (2000). Functional genomic analysis of *C. elegans* chromosome I by systematic RNA interference. Nature 408, 325-330; Gonczy, P., Echeverri, G., Oegema, K., Coulson, A., Jones, S. J., Copley, R. R., Duperon, J., Oegema, J., Brehm, M., Cassin, E. et al. (2000). Functional genomic analysis of cell division in *C. elegans* using RNAi of genes on chromosome III. Nature 408, 331-336; Maeda, I., Kohara, Y., Yamamoto, M. and Sugimoto, A. (2001). Large-scale analysis of gene function in *Caenorhabditis elegans* by high- throughput RNAi. Curr Biol 11, 171-176). Much of this data and all of the sequences are available through WormBase (~~http://www.~~ wormbase.org/). To date, over 2033 genes have been found to have an embryonic lethal RNAi phenotype and over 573 have a sterile RNAi phenotype. As described in more detail below and in the examples, these sequences may be screened for oral activity when expressed in plant tissue. In other embodiments, genes from this group that are specific to nematodes are utilized for RNAi so as to minimize interactions against endogenous proteins of plants, livestock and humans.

Please amend the Specification at page 34, line 22 through page 35, line 7 in the following manner:

Accordingly, in some embodiments, the present invention utilizes RNAi genes encoding dsRNA sequences that target nematode genes identified as having embryonic lethal or sterile RNAi phenotypes as identified by feeding nematodes dsRNA. The coding sequences for the target RNAs are available in public databases, including wormbase (~~www.~~wormbase.org). In still further embodiments, the genes utilized for RNAi are selected from the group consisting of major sperm protein, chitin synthase, and RNA polymerase II. The methods and compositions of

the present invention have been exemplified for the control of *H. glycines*. However, it will be recognized that these materials and methods can be used the control of other nematodes. Accordingly the present invention provides the sequences for *H. glycines* major sperm protein (e.g., SEQ ID NO:1), chitin synthase (e.g., SEQ ID NO:18), and RNA polymerase II (e.g., SEQ ID NO:9). As described above, the entire coding sequence of the genes can be used to make dsRNA for RNAi, or, alternatively, subsequences can be utilized. The following table presents other suitable subsequences for use in RNAi. Both these sequences and their complements are expressed from vectors as described herein to form double stranded RNA molecules.

Please amend the Specification at page 52, line 24 through page 53, line 9 in the following manner:

This Example describes the construction of an RNA polymerase II RNAi gene. Degenerate primers were used to retrieve RNA polymerase II sequence from *H. glycines*. Since *H. glycines* RNA polymerase II sequence was unknown, the primers had to be designed using sequence from *C. elegans* and three other related organisms-*Artemia salina* (brine shrimp), *Helobdella stagnalis* (leech), and *Ilyanassa obsolete* (eastern mud snail). The RNA polymerase II sequences of these four organisms were copied into Blockmaker (~~http://www.~~blocks.fhcrc.org). The blocks formed from Blockmaker were then copied into Codehop to make degenerate primers. The sequences were also copied into Clustalw, which, like Blockmaker, is a multiple sequence alignment tool. The advantage of using Clustalw is that it provides a view of the entire alignment of the sequences rather than just blocks of alignments. Clustalw also points out regions of the alignment that have very tight homology throughout the different organisms. Codehop constructs degenerate primers from the blocks assembled in Blockmaker. Degenerate primers were chosen that had tight homology in the sequence alignments in Clustalw, a GC content greater than 45%, degeneracy no greater than 16, and amino acids in the 3' end of the primer that are coded for by only 1 or 2 codons.

Please amend the Specification at page 53, line 24 through page 54, line 4 in the following manner:

SEQ ID NO:9 was used in a blastx search which compared it to a protein database (~~http://www.~~ncbi.nlm.nih.gov/BLAST/). The blastx search confirmed that the sequence of clone

6 was RNA polymerase II. Tblastx was also used which blasted the degenerate nucleotide sequence against a translated database. Tblastx aided in the location of exons and introns in the degenerate sequence. It was necessary to locate the exon regions of the sequence because the construct must be designed from regions that are transcribed (i.e. exons). From tblastx, it was estimated that an exon occurred between base pair 555 and base pair 834 in the degenerate sequence. This 279 base pair exon region is provided in Figure 6 as SEQ ID NO:10. This exon sequence was blasted against a protein database (blastx) to confirm that the exon was RNA polymerase II and also against the translated database (tblastx) to insure that the sequence was indeed an exon.

Please amend the Specification at page 56, lines 3-22 in the following manner:

This Example describes the construction of a chitin synthase RNAi gene. Chitin synthase gene was selected because in RNAi experiments by Piano et al. (Piano F, Schetter AJ, Mangone M, Stein LD, Kemphues KJ. RNAi analysis of genes expressed in the ovary of *Caenorhabditis elegans*. Current Biology 10: 1619) showed that silencing of this gene prevents development of nematode progeny (i.e. embryo lethal). The spliced sequenced together with Blockmaker (~~http://www.~~blocks.fhcrc.org), Codehop, and Clustalw to make degenerate primers and amplify the chitin synthase sequence from *Heterodera glycines*. This sequence is providing in Figure 12 (SEQ ID NO: 18). Sense and antisense fragments are cloned from the underlined region using methods similar to those described above. The sense and antisense fragments are then cloned into vector as described in Example 2. Primers useful for cloning the sense and antisense sequences include the following:

CHSY151_F: CCGATGCTTAGGCTGAC (SEQ ID NO:19)
CHSY210_F: CCAGCGGCAGTGATTC (SEQ ID NO:20)
CHSY287_R: AGCACACCTTCTCCAATC (SEQ ID NO:21)

CHSY355_F: TGGTACCAAAAGTTCGAGTAC (SEQ ID NO:22)
CHSY409_F: CATGTGTTCGGCTGTGT (SEQ ID NO:23)
CHSY543_R: ATCGGGTCTTCGCCTTG (SEQ ID NO:24)